Electronically Filed On: May 15. 7007

PATENT Attorney Docket No. 34170-701.501

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application:

Inventor: Peter S. Lu et al.

Application No.: 10/630,590

Filed: July 29, 2003

Title: METHODS OF DIAGNOSING

CERVICAL CANCER

Confirmation No.: 4993

Examiner: Lucas, Zachariah

Group Art Unit:

1648

Customer No. 21971

DECLARATION UNDER 37 C.F.R. §1.131

We, Peter S. Lu, Johannes Schweizer, Chamorro Somoza Diaz-Sarmiento, and Michael P. Belmares, declare as follows:

- 1. We are the inventors of claims 1, 3-8, 10-22 and 24-28 of the patent application identified above and the inventors of the subject matters described and claimed therein.
- 2. We conceived and reduced to practice in this country the invention claimed in claims 1, 3-8, 10-22 and 24-28 in the above-referenced application prior to September 6, 2001.
- 3. Prior to September 6, 2001 we conceived that the E6 protein of oncogenic human Papillomavius (HPV) has a C-terminal domain with a consensus sequence of -X-(S/T)-X-(V/I/L) that should be recognized and specifically bound to by a PDZ domain, such as domain 2 of MAGI-1, while non-oncogenic or low risk HPV E6 sequences should not. We developed assays to assess the binding interactions between the C-terminal domain of E6 protein of various oncogenic and non-oncogenic strains of HPV, such as the "G Assays" described in above-referenced application

serial No. 10/630,590 at pages 43-46, and in provisional application No. 60/309,841 filed on August, 3, 2001 at pages 32-36.

Prior to September 6, 2001 we designed and purchased from commercial suppliers peptides (see Exhibit A for evidence of purchase with dates obscured) containing the consensus C-terminal sequences derived from various oncogenic strains of HPV, and C-terminal sequences from non-oncogenic strains of HPV. Table 1 below lists the sequences of such peptides with the C-terminal consensus sequences of oncogenic strains of HPV highlighted in bold. As listed in Table 1, besides peptides which have the native sequences of the C-termini of the HPV strains, we also designed peptides that are derived from the native sequences of the C-termini by substituting amino acid residues (especially cysteine residues) outside the consensus 4 amino acid C-terminal sequences with other amino acid residues to avoid complications resulting from aberrant folding of the native peptides due to cross-linking of the cysteine residues that causes aggregation of the peptides. See designed peptide sequences labeled with "(modified)" or "(cysteine-free)" in Table 1.

Table 1. Sequences of C-terminal peptides derived from E6 protein of various HPV strains.

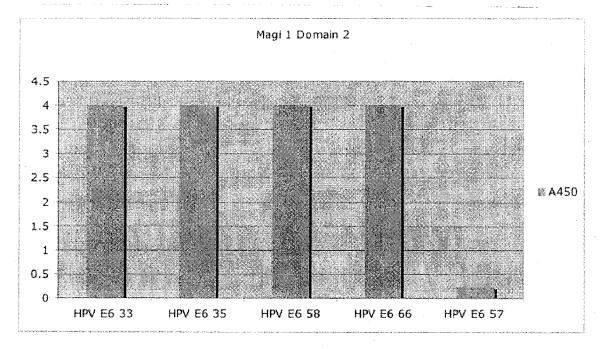
AVC Name	Sequence	oncogenic
HPV E6 16	WTGRCMSCCRSSRTRRETQL	Y
HPV E6 16 (Modified)	TGRGMSGGRSSRTRRETQL	Y
HPV E6 18	HSCCNRARQERLQRRRETQV	Y
HPV E6 18 (Modified)	SGGNRARQERLQRRRETQV	Y
HPV-E6 31	GRWTGRCIACWRRPRTETQV	Y
HPV E6 33	CAACWRSARRRRLQRRRETAL	Y
HPV E6 33 (modified)	aaggrsarggrlogrr eta l	Y
HPV E6 35	GRWTGRCMSCWKPTRRETEV	Y
HPV E6 35 (cysteine-free)	GRWIGRAMSAWKPTRRETEV	Y
HPV E6 36 (cysteine-free)	RVRNAWKGIARQAKHFYNDW	N
HPV-E6 51	CANCWORTRORRLORRNETOV	Y
HPV E6 52	MGRWTGRCSECWRPRPVTQV	Y
HPV E6 52 (modified)	SEGGRPTRGPRLQGRR VTQV	Y
HPV E6 57	HCMNCAPRCMENAPALRTSH	· N
HPV E6 57 (cysteine-free)	HAMNAAPRAMENAPALRTSH	N_
HPV E6 58	GRWTGRCAVCWRPRRRQTQV	Y
HPV E6 58 (modified)	AVGGRPARGGRLQGRRQTQV	Y
HPV E6 63	VHKVRNKFKAKCSLCRLYII	N
HPV-E6 66	TGSCLQCWRHTSRQATESTV	Y
HPV E6 66 (cysteine-free)	TGSALQAWRHTSRQATESTV	YY
HPV-E6 70	RHCWTSNREDRRRIRRETQV	Y
HPV-E6 77	GHWRGSCLHCWSRCMGQSRQ	N
HPV E6 77 (modified)	GGGRGSGLAGGSRGGGQSRQ	N
HPV-E6 80	QFHKVRRNWKGLCRHCGSIE	N

- 5. Prior to September 6, 2001 we used the G Assays to assess the interactions of peptides (Table 2) derived from the C-terminal 19-20 amino acids of E6 protein from oncogenic HPV types 33, 35, 58, 66 and non-oncogenic type 57. Peptide concentrations used in the G-assay were 10 uM, 1 uM, 10 uM, 3 uM, and 10 uM, respectively. Figure 1 summarizes the results of these experiments with the C-terminal consensus sequences of oncogenic strains of HPV highlighted. The absorbance value at 450 nm indicates the amount of HPV peptides bound to MAGI-1 domain 2. Exhibit B is a copy of pages from lab notebooks recording such experiments on which the dates have obscured.
- 6. As shown in Figure 1, prior to September 6, 2001 we demonstrated that all four of peptides derived from the E6 protein of oncogenic HPV strains 33, 35, 58 and 66 bound MAGI-1 PDZ domain 2 strongly at 1-10 uM peptide concentrations. In contrast, the E6 sequence from non-oncogenic HPV type 57 did not bind to MAGI-1 domain 2. In addition, peptides derived from the E6 protein of oncogenic HPV strains 16 and 18 that share the same consensus C-terminal sequence as strains 33, 35, 58 and 66 were later demonstrated to bind to MAGI-1 domain 2. Thus, since the claimed invention is a method or system for detecting the presence of an oncogenic HPV in a sample by using a PDZ domain polypeptide of less than 1000 amino acids in length and comprising the amino acid sequence of MAGI-1 PDZ domain 2, the claimed invention was conceived and reduced to practice prior to September 6, 2001.

Table 2. Sequences of C-terminal peptides derived from E6 protein of various HPV strains.

HPV Type	E6 C-terminal sequence	Derived from Oncogenic HPV E6
HPV 33 (modified)	AAGGRSARGGRLQGRR ETAL	Y
HPV 35 (cysteine-free)	GRWTGRAMSAWKPTRRETEV	Y
HPV 58 (cysteine-free)	AVGGRPARGGRLQGRRQTQV	Y
HPV 66 (cysteine-free)	TGSALQAWRHTSRQATESTV	Y
HPV 57 (cysteine-free)	HAMNAAPRAMENAPALRTSH	N

FIGURE 1: Binding strength of HPV E6 peptides with PDZ domain 2 of MAGI-1



7. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 05/(0/2007)

By:

Peter S. Lu, M.D.

Country of Citizenship: U.S.A.

By:

Johannes Schweizer

Country of Citizenship: Germany

Date: 5/8/07

By: Chamorro Somoza Diaz-Sarmiento Country of Citizenship: Spain

By: Michael P. Belmares Country of Citizenship: U.S.A.

U.S. Appl. Serial No. 10/630,590

Tel: 650-952-8193 Fax: 650-952-9540 www.genemedsyn.com 213 East Grand Avenue, South San Francisco, CA 94080 U.S.A

Genemed Synthesis, Inc.

PLEASE SEE ATTACHED FOR QUALITY CONTROL DATA

Custom Peptide Synthesis

Certificate of Analysis

Sequence:

N. End: Biomi

'N'--TGR / GMS / GGR / SSR / TRR / ETQ

Length: 19

7-7

C End:

AA69.1

Sequence Name:

Research

Scale:

20:0

0.0

Analysis:

Channel A

Peak No.

Time

14.255

Type

* HPLC Analysis:

* Amino acid

Quantity:

20 mg 2.62x 10 mmole

Form: Lyophilized powder

Molecular Weight:

1,094

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Storage and Stability:

Stable for one year at -20 °C.

Lot No.

10017449

* Mass spectroscopy

Height(μV)

Area(µV-sec)

6235630

6235630

Area%

100.000 100.000

Total Area

N4

196364

Data: 0-100 pepanal-

006

Sample:

17449 25µL injecteu

Column: Vydac C18 1ml/min

Buffers: A=0.1%TFA; B=0.1%TFA in CH3CN

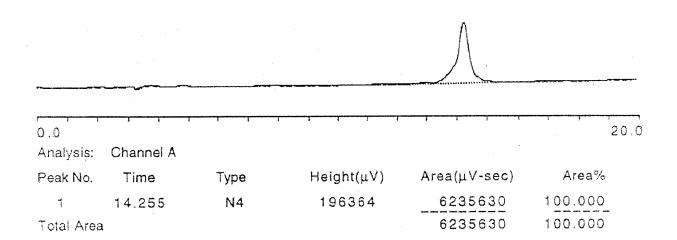
Gradient: 0-100%B, 20' Monitor: 220nm, 1.0 AUFS

Processing File: profile#1
Method: 0-100 pepanal

Inject Vol:

Sampling Int: 0.1 Seconds

Data:



FOR RESEARCH USE ONLY. Not for diagnostic and medical applications

Custom Peptide Synthesis Certificate of Analysis

	Sequence:		Sequence Name:	
'N'SGG/NRA/RQE/RLQ/RRR/ETQ/	'N' End: Biotin		AA70.1	
QE/RLQ/			Scale:	
RRR/ETQ/		And the second s	Research	

Length: 19

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Molecular Weight: をなる -2,298 るらって

"C' End:

To mg Tilly mmole

Form: Lyophilized powder.

Quantity:

Analysis:

* HPLC

* Amino acid

* Mass spectroscopy

Storage and Stability: Stable for one year at -20 °C.

Lot No. 10017450

PLEASE SEE ATTACHED FOR QUALITY CONTROL DATA

Genemed Synthesis, Inc.

213 East Grand Avenue, South San Francisco, CA 94080 U.S.A. Tel: 650-952-8193 Fax: 650-952-9540 www.genemedsyn.com

Scans Averaged: 61 Laser: 2230

Pressure: 6.61e-07

Low Mass Gate: OFF

Negative 15

Timed Ion Selector: 15,1 OFT PSD Mirror Ratio Mirror Ratio: 1.070

Date:

Data: 0-100 pepanar-

-016

Sample:

17450 **25**µl injected

Column: Vydac C18 1ml/min

Buffers: A=0.1%TFA; B=0.1%TFA in CH3CN

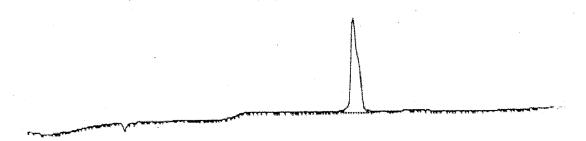
Gradient: 0-100%B, 20' Monitor: 220nm, 1.0 AUFS

Processing File: profile#1 Method: 0-100 pepanal

Inject Vol:

Sampling Int: 0.1 Seconds

Data:



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Analysis:	Channel A				
Peak No.	Time	Type	Height(μV)	Area(μV-sec)	A:
1	10.780	Ν	96091	1355988	100
Total Area	4			1355988	100

213 East Grand Avenue, South San Francisco, CA 94080 U.S.A.

Genemed Synthesis, Inc.

Tel: 650-952-8193 Fax: 650-952-9540 www.genemedsyn.com

Custom Peptide Synthesis Certificate of Analysis

Data:

Sampling Int: 0.1 Seconds

Inject Vol:

Method: 0-100 pepanal profile#1 Processing File:

7 Monitor: 220nm, 1.0 AUFS Gradient: 0-100%B, 50. 17517 25µl injected Column: Vydac C18 1ml/min Buffers: A=0.1%TFA; B=0.1%TFA in CH3CN

Sample:

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Sequence Name: Sequence: Molecular Weight: Length: 20 'N'--AAG / GRS / ARG / GRL / QGR / RET / C End: 'N' End: Biotin はます AL - 'C' AA72.1 1200 A 1200 KM Scale: Research

Analysis:

Form: Lyophilized powder

Quantity:

Zo mg LLYLommole

* HPLC

* Amino acid

* Mass spectroscopy

Lot No.

10017517

PLEASE SEE ATTACHED FOR QUALITY CONTROL DATA

Storage and Stability: Stable for one year at -20 °C.



Certificate of Analysis

Peptide Name:	AA80.1
Run Number:	17702
Sequence:	Biotin-Gly-Arg-Trp-Thr-Gly-Arg-Ala-Met-Ser-Ala-Trp- Lys-Pro-Thr-Arg-Arg-Glu-Thr-Glu-Val-OH
Theoretical Mass(M+H ⁺)	= 2603.0 2600.51
Mass Found(M+H*):	2602.3
Solubility:	Dissolve 1mg of peptide in 1ml Water
Appearance:	White Powder
HPLC Purity:	>*N/A %
Amount Delivered:	100 mg *Customer requested unpurified peptide
Storage :	Keep Refrigerated
Remarks: Not for	or Human Use. Research Purposes Only.
Release By:	aswinder Kavi Date: Quality Control

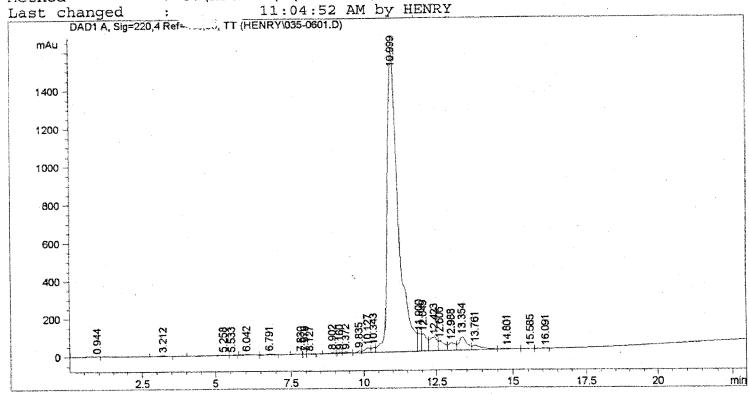
Data File C:\HPCHEM\1\DATI ENRY\035-0601.D

Sample Name: AA80.1

Injection Date : Seq. Line : 6
Sample Name : AAoU.1 Vial : 35
Acq. Operator : HENRY Inj : 1

Different Inj Volume from Sequence ! Actual Inj Volume : 5 μ 1 Actual Inj Volume : 2 μ 1

Sequence File : C:\HPCHEM\1\SEQUENCE\DEF_LC.S
Method : C:\HPCHEM\1\METHODS\0-100-20.M



Area Percent Report

Sorted By : Signal Multiplier : 1.0000 Dilution : 1.0000

Signal 1: DAD1 A, Sig=220,4 Ref=450,80, TT Results obtained with standard integrator!

Peak #	RetTime [min]	Туре	Width [min]	Area [mAu*s]	Height [mAu]	Area %
1 2 3 4 5 6 7 8 9	0.944 3.212 5.258 5.533 6.042 6.791 7.830 7.979 8.127 8.902 9.160	VB BV PV PV VV VB PV	1.0963 0.2199 0.3324 0.1817 0.1638 0.1581 0.2492 0.0858 0.1281 0.1558 0.1115	27.31302 65.38581 38.73496 8.00819 48.28724 51.54432 13.29615 3.90877 7.46610 68.03886 43.50458	2.94576e-1 4.18458 1.52027 7.34552e-1 4.21066 4.71076 6.67421e-1 6.33285e-1 7.92417e-1 5.92069 5.49541	0.0558 0.1336 0.0792 0.0164 0.0987 0.1053 0.0272 7.988e-3 0.0153 0.1390 0.0889

EXHIBIT A CONTINUED

Custom Peptide Synthesis

Certificate of Analysis

Sequence Name:

Scale: Research

Sequence:

N End: Diotie

Length: 20

N'--AVG / GRP / ARG / GRL / QGR / RQT / QV -- 'C

C End:

347 2345, 49

Molecular Weight: Quantity:

20 mg 051410 mmole

Form: Lyophilized powder.

Analysis:

- * HPLC
- * Amino acid
- * Mass spectroscopy

Storage and Stability: Stable for one year at -20 °C.

Lot No. 10017523

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FOR RESEARCH USE ONLY. New for diagnostic and medical applications

Mass (m/z)

Laser: 2190

Scans Averaged: 12

PSD Mirror Ratio: 1.070

Pressure: 8,00e-07

Low Mass Gate: OFF

Negative lons: OFF

7.ms
3007.MS
Collected. 10.31 AM Sample 45

20.0

Date:

Data: c .J0 pepanal-

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Sample:

17523 25μl injected

Column: Vydac C18 1ml/min

Buffers: A=0.1%TFA; B=0.1%TFA in CH3CN

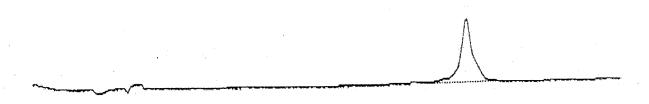
Gradient: 0-100%B, 20' Monitor: 220nm, 1.0 AUFS

Processing File: profile#1 Method: 0-100 pepanal

Inject Vol:

Sampling Int: 0.1 Seconds

Data:



0.0 Analysis: Channel A Area(µV-sec) Area% $Height(\mu V)$ Peak No. Time Туре 100:000 14.721 N11 112398 3014595 100.000 Total Area



Certificate of Analysis

Peptide Name:	AA66.1				
Run Number:	17700				
Sequence:	BIOTIN-Thr-Gly-Ser-Ala-Leu-Gln-Ala-Trp-Arg-His- Thr-Ser-Arg-Gln-Ala-Thr-Glu-Ser-Thr-Val-OH				
Theoretical Mass(M+H ⁺):	2414.7				
Mass Found(M+H*):	2414.3				
Solubility:	Dissolve 1mg of peptide in 1ml Water				
Appearance:	White Powder				
HPLC Purity:	>*N/A %				
Amount Delivered:	100 mg *Customer requested unpurified peptide				
Storage :	Keep Refrigerated				
Remarks: Not fo	r Human Use. Research Purposes Only.				
Release By:	Jaszonden Kanr Date:				
	Quality Control				

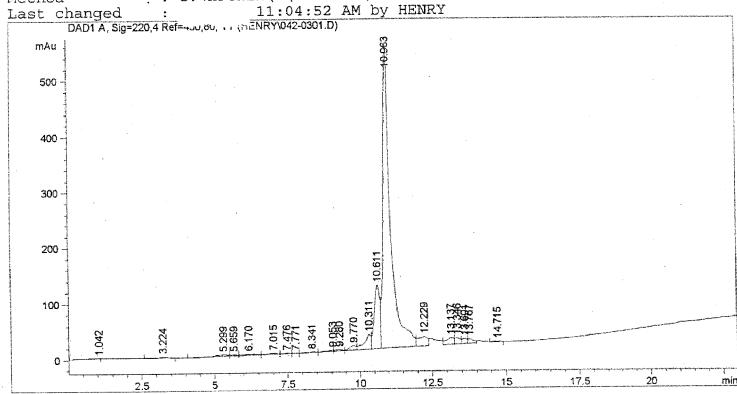
Sample Name: AA66.1

Injection Date : 7:47:03 PM Seq. Line : 3 Sample Name : AAo6.1 Vial : 42 Acq. Operator : HENRY Inj : 1 Inj Volume : 5 μ l

Different Inj Volume from Sequence ! Actual Inj Volume : 2 μ l

Sequence File : C:\HPCHEM\1\SEQUENCE\DEF_LC.S

Method : C:\HPCHEM\1\METHODS\0-100-20.M



Area Percent Report

Sorted By : Signal Multiplier : 1.0000 Dilution : 1.0000

Signal 1: DAD1 A, Sig=220,4 Ref=450,80, TT Results obtained with standard integrator!

Peak I	RetTime [min]	Туре	Width [min]	Area [mAu*s]	Height [mAu]	Area %
 1 2 3 4 5 6 7 8 9 10	1.042 3.224 5.299 5.659 6.170 7.015 7.476 7.771 8.341 9.053 9.280	BV BV VV VV	3.5187 0.2008 0.3742 0.2618 0.4283 0.2753 0.1824 0.1100 0.1796 0.2286 0.2323	29.64368 29.17170 87.51175 37.78679 68.21159 40.34123 12.75530 3.22723 12.61311 44.93953 45.01051	1.00569e-1 1.88686 2.88747 2.13710 1.91198 1.83774 9.23668e-1 3.85199e-1 1.15197 2.49896 2.51241	0.2185 0.2151 0.6452 0.2786 0.5029 0.2974 0.0940 0.0238 0.0930 0.3313 0.3318

Vitnessed & Understood by me,

Date/Initials

Reagents and Supplies

Transtar Costar# Cluster tubes

SoftMax Pro software

Recorded by Morles

Book No. 164

175×6 13A TITLE ___

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0001A-NOSS
0001A-NOSS AA178RA-GEF (HAMIDIA AAST.1849V ES 657 (HYDI AACIDICATERINI (MANANI AACIDILATIKA (MANANI AA172/FA-GEF (revise) A AA67_1/HPV E6 867 (cycle) AAGE, TOLLIFIZ general AAT72/FA-CIEF (mahmpi AAR7, IMPV 66 667 (uptai AA72, IMPV 66 68 (madile AA75, IMPV 66 68 (madile AAGE/Fapper's (makes) AAT08, TAZLIFIZ (gluberal) 0.264 1.625 0.133 0.260 4 4 0.328
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PRISM Matrix ELISA G Assa,	POST IN E	
Date/Initials 8/7/01 KC, BK	PEPTIDE	
	1234561	2 3 4 5 6
Reagents and Supplies Nunc Polysorp 96 well immuno-plate, Nunc cat#62409-005 batch# 045987. Nunc Polysorp 96 well immuno-plate, Nunc cat#62409-005 batch# 045987. Nunc Polysorp 96 well immuno-plate, Nunc cat#62409-005 batch# 045987.	i 2 3 4 5 6 7	8 9 10 11 12
PBS per /- Universities of AVC local 97 -93-04	A PROTEIN 1	
Assay Buffer: 2% BSA in PBS (20g of bovine serum audumn pc) in the post in the	B PROTEIN 2	-+-+-+-
Goat anti-GST polyclonal Ab, stock 5 mg/ml, stored at 4°C, Amersham Financial	C PROTEINS	
e Dilute 1:1000 in PBS, final concentration 5 µg/ml. Date preparet. HRP-Streptavidin, 2.5mg/2ml stock stored @ 4°C, Zymed cat#43-4323, lot# 101 to 2469	D PROTEIN 4	
HRP-Streptavidm, 2.5mg/2mi stock stated 4 5, 25		
dilute 1:2000 into Assay buffer, mai [0.3 µg/mi] Wash Buffer, 0.2% Tween 20 in 50mM Tris pH 8.0, AVC lot# 97-96-02 Biotinylated peptides (HPLC purified, stock solution store in -20°C freezer #7)		
e GST-PRISM proteins (stock stored @ -80°C, after 1" maw store in -10 C 10021 11/100	F PROTEING	
0 18M H-SO. Sigma cat.#S1526, AVC 101#	G EST + KINKER CONTROL	
12-w multichannel pipettor & tips 50 ml reagent reservoirs, Costar#4870	H STANDARD CORVE ST	ANDARD CURVE
50, 15 ml polypropylene conical tubes Contr Transtar 96 Costar#7605		
Transtar 96 Cartridge Costar#7610 Transtar Costar#		
Cluster tubes Molecular Devices microplate reader (450 & 650 nm filters)	Standard Cur	
·		4, 10 5, 11 6, 12
SoftMax Pro software When using reagents stored at or 4°C or -20°C, remove & keep on ice		A 0.067µM 0.016µM 0.004µM
 Protocol Coat plate with 100 μl of 5 μg/ml anti-GST, O/N @ 4°C 		
Coat place with 100 plate & out tap dry on paper towels Add 200 µl Assay Buffer for 2 hrs at 4°C Add 200 µl Assay Buffer for 2 hrs at 4°C	196 1193	16
4. Prepare proteins and peptides in Assay Butter	100	
6 Add proteins at 50 ul per well, incubate 1 to 2 hrs at 4 C		1.11 10 -10
Wesh 3X with cold PBS* Add peptides at 50 µl per well on ice (write time on plate) Add peptides at 50 µl per well on ice (write time on plate)	362) Newrolingles	in - differently mode
Add peptuces at 50 m per weat in 60 (when a first peptide has been added for exactly 10 minutes Diaco at room temp for exactly 20 minutes	36.3 / biotinglas	ed peptides for companion
11. Prepare HRP-Streptavidin within 10 minutes of time of use 12. Promptly wash 3X with cold PBS	80.1 HPV26	
13. Add 100 µl per well of HRP-Streptavidin (write time on plate) 14. Incubate at 4°C for exactly 20 minutes	to the S. A. Commission of the	
15. Turn on plate reader and prepare files (store as 010501 fkt) 16. Promptly wash 5X with Wash Buffer		
17. Add 100 μl/well TMB substrate (write time on piace)	000 Berotonin	10:
 incubate in dark at 100 in telling the control of the	258 Noradren	rline
21. Take last reading at 450 nm soon after stopping reaction • Leave last PBS in wells until ready for next step,		
i.e. do not let plates dry out		
	The second of	
	Approximation of the second se	
I I I I I I I I I I I I I I I I I I I	The second secon	To Page No.
With a good & Linderstood by me. Date	invented by	Def#
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Maryonie James		ク!
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TITLE	186×611N	Book No. <u>/57</u>	87
Proto # 1303 Croation Date Creation To 80:20:20 1:08 Col. Rew Frolden 1:1 A 7750AA356A 2 2 A A 7750AA356A 3 A 7750AA356A 4 A A 7750AA356A 6 S A 7750AA356A 6 S A 7750AA356A 7 T A 7750AA356A 7 T A 7750AA356A 10 10 B 7750A	### Arbor Vita Corp. CONFIDENTIAL Time Street Street Prop. Prop. Appl. Ap	Part	0 0.005 0 0.075 0 0.075 0 0.075 0 0.064 0 0.064 0 0.067 0 0.067 0 0.067 0 0.067 0 0.067 0 0.067 0 0.067 0 0.067 0 0.067 0 0.068 0 0.077 0 0.077 0 0.077 0 0.077 0 0.077 0 0.077
6 6 6 6000T 9 6 6000T 1 6 6000T 1 7 6 6000T 1 7 6000T 1 8000T 1 1 6000T 1 1	9 E AASTECECRS (HEV CO-mos 883 10 9 E AASSC/Seculation recorptor 880 9.7	0 0.167 70 8 0 8406T 9 5 AASECHOUGHOUGHO NON 200 10 1,000 70 7 0 8406T 9 6 AASECHOUGHOUGHO NON 200 10	0 0.771 0 0.086 0 0.077 0 0.086 0 0.076 0 0.186 0 0.756 0 0.756 0 0.186 0 0.066 0 0.066 0 0.066 0 0.066 0 0.066 0 0.066 0 0.066 0 0.066 0 0.066

EXHIBIT B-

Project No.__

21 9×18 8.1A Book No. m Page No. <u>20</u> Plate # 1651 Tempiste 450 .. 17:10:15 17:10:18 0,107 0,10 2,84 8,16 8,00 ААААААААААААААА Frap Prot. 00 0.043 0.173 0.00 0.000 0.106 0.000 0.106 0.236 0.073 0.136 0.572 0.002 4 0.277 0.206 0.246 0.274 Protein 79/7/102 (Libe Protein) | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 72/TAX2 (ibs Protein)
72/TAX2 (ibs Protein) AA177L/o-bb room AA180A9ADA Ghr 10News POZ 10News POZ AA177L/mill sedente AA177L/mill sedente AA180Hill/IA Obdance AANA 1860Y Es oos in SOPienei POZ AARE 10-PY E6 900 IN 8.08 9,146 9,298 9,176 9,250 9,151 TOTALE (Lin Pr TOTALE (Lin Pr AMELINEY ET PRE Joy 17/Moni POZ
17/Mon 0.111 0.161 0.16 AANS. 10-PV ES 000 (m) 0.156 0.006 0.006 0.106 0.264 0.901 0.884 0.143 0.448 0.104 0.209 0.105 0.100 0.100 0.107 0.107 0.107 0.107 0.107 0.106 0.000 0.000 0.106 AAGS THEY ES SOO (97 0.14 0.00 0.190 0.14 0.12 0.125 0.680 0.144 0.167 0.277 0.147 0.277 0.147 MAR. 1957 E4 694 A THIRDATION
THIRDATION 4 0.175 8.146 8.839 8.203 8.107 0.303 0.303 9,104 9,891 9,121 9,146 9,176 9,076 9,105 0.197 0.364 0.570 0.138 0.186 0.29 0.147 0.138 0.138 0.001 0.675 0.003 1.741 0.772 0.201 0.922 0.14 0.072 1.767 0.269 0.269 0.072 AA64, VHPY SI 866 (= 0.144 0.19 0.172 2.361 0.297 0.117 0.112 1.866 1.005 0.273 0.273 0.273 0.273 0.411 0.416 0.416 0.416 0.416 AABUTAX To Page No. 82 Date Invented by Date essed & Understood by me, Cariporie Junes

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